SEARCH REQUEST FURM

| Requestor's Name: | | Serial Number: | |
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| Date: | Phone: | | Art Unit: |
| terms that may have a special | meaning. Give examples or re | specifically as possible the subjection of the broadest and/or most | ect matter to be searched. Define any vords, etc., if known. For sequences, relevent claim(s). |
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STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 102216

To: Minh-Tam Davis

Location: CM1-8E12

Art Unit: 1642

W dnesday, August 27, 2003

Cas Serial Number: 09/700700

From: Beverly Shears

Location: Biotech-Chem Library

CM1-1E05

Phone: 308-4994

beverly.shears@uspto.gov

Search Notes

pronty date: 05/21/98



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GenCore version 5.1.6
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August 26, 2003, 12:08:16; Search time 9197 Seconds (without alignments) 8611.617 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

US-09-700-700-1 1936 Perfect score:

1 aatggtatgccaacttaagt.......ggggcggccgccgactagtga 1936 IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table: Sequence:

2888711 segs, 20454813386 residues Searched:

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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:* Database

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SUMMARIES

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2984 bp DP Sequence 335 from patent US 6465611. AR237420 AR237420.1 GI:27282078 Unclassified. Unknown. Unknown RESULT 1
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ALIGNMENTS

1 (bases 1 to 2984) Xu,J., Dillon,D.C. and Mitcham,J.L. Compounds for immunotherapy of prostate cancer and methods for their use Patent: US 6465611-A 335 15-OCT-2002; REFERENCE AUTHORS TITLE JOURNAL

| PERTURBES LICORELION/QUAILITIES SOUTHON SOUTHON STATEMENT OF A PROPERTY OF STATEMENT OF STAT | 1102 GAGANGCONGTITATTGCCTATAATGGGTCCCCAAATGGGTAACCTGGACTTCAGA 102 GAGANGCONGTGCTATAATGGGTCCCCCAAATGGGTAACCTGGACTTCAGA 103 GAGANGCONGAGANAGGAGAAATCTGGCTGCCTCCCTTTTTTTTTTTT | Db 2920 ACATATGAGTGTTTTGAAAATAAAGTACCCATGTCTTTATTAGAAAAAAAA |
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CE 1 (bases 1 to 2984)
JRS Mashiki,Z. and Harada,J.
B. Negative pressure control apparatus for engine mounted in value Patent: US 6321716-A 335 27-NOV-2001;
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| 1545 CAAAGCTTTATCTGTCTTTTTAAAAAAGTTTGGGGGCAGATTCTGAATT-GGCTA 1603 541 AAAGACATGCATTTTTAAAACTAGGCAACTTCTTATTTCTTTTCTTTAAAAATACATAGC 600 | | 601 AITAAATCCCAAAICCTAITTAAAGACCTGACAGCTTGAGAAGGICACTACTGCAITTAI 660 | 661 AGGACCTTCTGGTGGTTCTGCTGTTTGAAGTCTGACAATCCTTGAGAATCTTTGC 720 | 721 ATGCAGAGGAAGAGGTATTGGATTTTCACAGAGGAAGAACACAGCGCAGAATGAAG 780 | 781 GGCCAGGCTTACTGAGGCTGTCCAGTGGAGGCTCATGGGTGGACATGGAAAAGAAGGC 840 | 841 AGCCTAGGCCCTGGGGGCCCAGTCCACTGAGCAAGGAAGG | 901 AGGAAAGGCTAAGAAAAGGAAAACCATTCTAAAACACAACAAGAAACTGTCCAAATGC 960 | 961 TITGGGAACTGTGTTTATTGCCTATAATGGGTCCCCAAAATGGGTAACCTAGACTTCAGA 1020 | 1021 GAGAATGACCAGAGAGAGAAATCTGGCTGTCCTTCCATTTTCATTCTTTGTTATCT 1080 | 1081 CAGGTGAGCTGGTAGAGGGGGACATTAGAAAAAATGAAACAACAACAAAAAAAA | 1141 GAGGTACGCTGGGAGTCTCTTGACTCCACTAATTCCGTTTAGTGAGAAA 1200 2201 GAGGTACGCTGAGGCCTGGGAGTCTCTTGACTCCACTTAATTCCGTTTAGTGAGAAA 2260 | 1201 CCTTTCAATTTTCTTTATTAGAAGGCCAGCTTACTGTTGGTGGCAAAATTGCCAACAT 1260 | 1261 AAGTTAATAGAAAGTTGGCCAATTTCACCCCATTTTCTGTGGTTTGGGCTCCACATTGCA 1320 | 1321 ATGTTCAATGCCACGTGCTGACACCGACCGAGTACTAGCCAGCACAAAAGGCAGGG 1380 | 1381 TAGCCTGAATTGCTTTTTGCTTTTTTTTTTAAATAAGCATTTAGTGCTCAGTC 1440 [| 1441 CCTACTGAGTACTCTTTCTCCCCCTCTGAATTTAATTCTTTCAACTTGCAATTTGC 1500 1501 CTACTGAGTACTCTTTCTCTCCCCTCTGAATTTAATTCTTTCAACTTGCAATTTGC 2500 | 1501 AAGGATTACACTTTCACTGTGATGTATATTGTGTTGCAGNGAAAAGAAAA | 1561 TGTTTAAAATTACTTGGTTTGTGAATCCATCTTGCTTTTTCCCCATTGGAACTAGTCATT 1620 |
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| Db 2800 AATTAGTITGGGTTCTCTACATGCATAACAAACCCTGCTCCAATCTGTCACATAAAAGTC 2859 Qy 1801 TGTGACTTGAAGTTTAGTCAGCACCCCCACCAAACTTTATTTTTTTT | 2860 TGTGACTTGAAGTTTAGTCAGCACCCCCACCAAACTTTATTTTCTATGTGTTTTTTGC 291 | Oy 1861 ACATATGAGTGTTTTGAAAATAAAGTACCCATGTCTTTATTAAAAAAAA | T 4 211 | DOCUS ALLOS211 2984 bp DNA Linear PAT 30-APR-2001 DOCUS SEQUENCE 349 from Patent W00125273. ACCESSION AX106211. VERSION AX106211.1 GI:13921900 | KEYWCUSS SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | Mammalia; Eutheria; Primates; Skeiky,Y.A., Xu,J., Cheever,M. Compositions and methods for w | CORIXA CORPORATION (US) FEATURES CONICE 1. 2984 | $\begin{tabular}{lllllllllllllllllllllllllllllllllll$ | / Match | 1 AATGGTATGCCAACTTAAGTATTTACAGGGTGGCCCAATAGAACAAGATG | 61 TGATTTTAACACCAGGCTGTATAACACACACCACTGCAAGAGGGGGGGCGGGC | 121 GAATCTCCGCTTGTTCCAAGACGCGCCTAAGGAGGGTCTCCCACACTGCTGCTAGGGGCT 180 1187 GAATCTCCGCTTGTCCAAGAGGGCCTTAAGAGAGGGTCTCCACACTGCTGCTAGGGGCT 124 | GTTGCATTTTTTATTAGTAGAAAGTCGAAAGGCCTCTTCTCAACTTTTTTCCCTTGGGC 240 | TGTATCCT 300 | GAAAGGCAACATAATTCTTCCTTCCTTTTAAAATTTTGTGTTCCTTTTTGCAGCAA 360 | TTACTCACTAAAGGGCTTCATTTTAGTCCAGATTTTTAGTCTGGCTGCACCTAACTTATG 420 | CGTCTCCC | CAAAGCTTTAICTGTTTGACTTTTTAAAAAGTTTGGGGGGAGATTCTGAATTGGGCTA |

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Catarrhini, Hominidae, Homo.
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/organism="Homo sapiens"
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Mammalia; Eutheria; Primates;
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| ORIGIN Query Match Best Local Similarity 99.0%; Pred. No. 0; Matches 1897; Conservative 0; Mismatches 12; Indels 7; Gaps 5; | Oy 1 AATGGTATGCCAACTTAAGTATTTACAGGCTGGCCCAAATAGAACAAGATGCACTCGCTG 60 | acaagctgtataaacagaactccactgcaagagggggggg | 121 GAATCTCCGCTTGTCCAAGACGGCCCTAAGGAGGTCTCCACACTGCTGGTAGGGGCT | 181 1247 1247 | 1307 TGGAGAATTTAGAATCAGAAGTTTCCTGGAGTTTTCAGGCTATCATATATACTTTTTCTTTC | 301 GAAAGGCAACATAATTCTTCCTTCCTTTTAAATTTTGTGTGTTTTGCAGCAA 36 | 361 TTACTCACTAAAGGCTTCATTTTAGTCCAGATTTTTAGTCTGGCTGCACCTAACTTATG 1427 TTACTCACTAAAGGGCTTCATTTTAGTCCAGATTTTTAGTCTGGCTGCACCTAACTTATG 1427 TTACTCACTAAAGGGCTTCATTTTAGTCCAGATTTTTAGTCTGGCTGCACCTAACTTATG | | QY 481 CAAAGCTTTATCTGTCTTGACTTTTTAAAAAGTTTGGGGGCAGATTCTGAATTGGGCTA 540 | | OY 601 ATTAAATCCCAAATCCTATTAAAGACCTGACAGGTTGAGAGGTCACTACTGCATTAT 660 | 0y 661 AGGACCTTCTGGTGGTTCTGCTGTTAGAGTCTGACAATCCTTGAGAATCTTTGC 720 | QY 721 ATGCAGAGGTAAGAGGTATTGGATTTTCACAGAGGAAGAAGAAGGCCAGAATGAAG 780 INELLIC | 781 GGCCAGGCTTACTGAGGCTGTCCAGTGGAGGGCTCATGGGGGCAAAAGAAGGC 8 | 1842 | ACCTAGGCCTGGGGGAGCCCAGTCCACTGAGCAAGGAACGAAC | QY 901 AGGAAAAGGCTAAGAAAAAAGAAAAACCATTCTAAAACACAACAACAACAACAACTGTCCAAATGC 960 DD 1961 AGGAAAAGGCTAACAAAAAGGAAAACCATTCTAAAACAACAACAACAACAACAACAACAAC | 961 | Db 2021 TTTGGGAACTGTTTATTGCCTATAATGGGTCCCCAAAATGGGTAACCTAGACTTCAGA 2080 |
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of prostate
cancer
Patent: WO 0173032-A 335 04-OCT-2001;
CORIXA CORPORATION (US)
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                                                     1 AATGGTATGCCAACTTAAGTATTTACAGGGTGGCCCAAATAGAACAAGATGCACTCGCTG
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others
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                      94.9%; Score 1836.4;
99.0%; Pred. No. 0;
iive 0; Mismatches
842
                      Query Match
Best Local Similarity 99.0
Matches 1897; Conservative
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DNA

AX267361 2984 bp Sequence 335 from Patent WO0173032. AX267361

AX267361.1 GI:16516135

Homo sapiens (human) Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

| Db 2920 ACALAIGAGIGITITGAAAAIAAAGIACCCAIGICITIAITAGAAAAAAAAAA | RESULT 9 AC012574/c LOCUS AC012574 B0586 bp DNA linear PRI 01-APR-2002 BEFINITUD Homo sapiens chromosome 8, clone RP11-213G6, complete sequence. | | ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | REFERENCE 2 (Dases 1 to 80586) AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguelavkly, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., | Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., | Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Moldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., | Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M. TITLE Direct Submission | JOURNAL Submitted (30-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA REFERENCE 3 (bases 1 to 80586) AUTHORS Birren.B., Linton.L., Nusbaum.C., Lander.E., Ali.A., Allen.N. | Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chararo, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S. | Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Grahlam,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kalis,C., LaRocque,K., Lamazares,R., | <pre>Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Mathews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Mirphy, T., Naylor, J., Nquyen, C., Nicol, R.,</pre> | Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Petcerson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R., | Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trajis, N., Trajis, N., Trajis, N., Travis, N., Tayanis, N. | Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. TITLE Direct Submission JOURNAL Submitted (01-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA | COMMENT On Apr 1, 2002 this sequence version replaced gi:15213914. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washindcon.edu/RW/RepeatMasker.html | Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIRR | Web Site: http://www-seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu |
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| 781 GGCCAGGCTTACTGAGGCTGTCCAGTGGAGGCTCATGGGTGGACATGGAAAAGAAGGC 840 | 841 AGCCTAGGCCCTGGGGAGCCCAGTCCACTGAGCAAGGAAGG | AGGAAAAGGCTAAGAAAAAGGAAAACCATTCTAAAACACAACAACAACAACTGTCCAAATGC | 961 TTTGGGAACTGTGTTTATTGCTTATAATGGGTCCCCAAATGGGGTAACCTGGACTTCAGA 1020 | 1021 GAGAATGAGCAGAGGAAAGGGAAATCTGGCTGTCCTTCCATTTTCATTCTGTTATCT 1080 | 1081 CAGGTGAGCTGGTAGAGGGGAGACATTAGAAAAAATGAAACAACAAAAAATACTAAT 1140 | OY 1141 GAGGTACGCTGAGGCCTGGGAGTCTCTTGACTCCACTACTTAATTCCGTTTAGTGAGAAA 1200 | 1201 CCTTTCAATTTTCTTTTAATAGGCCAGCTTACTGTTGGTGGCAAATTGCCAACAT 1260 | 1261 AAGTTAATAGAAAGTTGGCCAATTTCACCCCATTTTCTGTGGTTTGGGCTCCACATTGCA 1320 | 1321 ATGITCAATGCCACGTGCTGACCGACCGGAGTACTAGCCAGCACAAAAGGCAGG 1380 | 1381 TAGCCTGAATTGCTTTCTGCTCTTTACATTTTTAAAATAAGCATTTAGTGCTCAGTC 1440 | ACTGAGTACTCTTCTCCCCCTCCTGAATTTAAITCTTTCAACTTGCAATTTGC | 1501 AAGGATTACACATTTCACTGTGATGTATATTGTGTTGCAGNGAAAAGAAAA | 1561 TGTTTAAAATTACTTGGTTTGTGAATCCATCTTGCTTTTCCCCATTGGAACTAGTCATT 1620 | 1621 AACCCATCTCTGAACTGGTAGAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGG 1680 | TTCTATCCTGTTTAATA | 1741 AATTAGTTTGGGTTCTCTACATGCATAACAAACCCTGCTCCAATCTGTCACATAAAAGTC 1800 | AGTCAGCACCCCACCAAACTTTATTTTCTATGTGTTTTTTGCA | |

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                                                     Only the first 80.6 kilobases of this clone is being submitted. The remainder overlaps either accession number AC051642 [WICGR project L8828] or accession number AC012119 [WICGR project L2190]. Location/Qualifiers
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omplement(13943. .14098)

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omplement (2701. 2738)
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| 121 GAATCTCCGCTTGTCCAAGACAGGGCCTAAGGAGGGTCTCCACACTGCTGCTAGGGGCT 180 10582 GAATCTCCGCTTGTCCAAGACAGGGCCTAAGGAGGTCTCCACACTGCTGCTAGGGGCT 10523 181 GTTGCATTTTTATTAGAAGAGAGAGAAGGCCTCTCTCAACTAACAAGGCCTCTAAGAAGGCCTCTAAGAAAGGCCTCTTCTCAAAGGCCTCTCAAAGGCCTCTAAGAAAGGCCTCTTCTCAAAGGCCTCTTCTCAAAGGCCTCTTCTCAAAGGCCTCTTCTCAAAGGCCTCTTCAAAGGCCTCTTCTCAAAGGCCTCTTCTCAAAAGGCCTCTTCTCAAAAGGCCTCTTCTCAAAAGGCCTCTTCTCAAAAGGCCTCTTCTCAAAAGGCCTCTTCTCAAAAGGCCTCTTCTCAAAAGGCCTCTCAAAAGGCCTCTTCTCAAAAGGCCTCTTCTCAAAAGGCCTCTTCTCAAAAGGCCTCTTCTCAAAAGGCCTCTTCTCAAAAGGCCTCTTCTCAAAAGGCCTCTTCTCAAAAGGCCTCTTCTCAAAAGGCCTCTTCTCAAAAGGCCTCTTCTCAAAAGGCCTCTTCTCAAAAGGCCTCTTCTCAAAAGGCCTCTTCTCAAAAAGGCCTCTTCTCAAAAAGGCCTCTTCTCAAAAAGGCCTCTTCTCAAAAGGCCTCTTCTCAAAAAGGCCTCTTCTCAAAAAGGCCTCTTCTCAAAAAGGCCTTCTCAAAAAGGCCTCTTCTCAAAAAAAA | | 10462 IGGAGAAITIAGAAICAGAAGITICCIGGAGITITCAGGCIAICAIAIATACIGIAICCI 10403 301 GAAAGGCAACATAAITCITCCTICCCTCCTITIAAAAITITGIGITCCTITITGCAGCAA 360 10402 GAAAGGCAACATAAITCITCCTICCTICCTITIAAAAITTIGIGITCCTITITGCAGCAA 10343 | 361 TTACTCACTAAAGGCCTTCATTTTAGTCCAGATTTTTAGTCTGGCTGCACCTAACTTATG 420 | 421 CCTCGCTTATTTAGCCCGAGATCTGGTCTTTTTTTTTT | 477 TCCCCAAAGCTTTATCTGTCTTGACTTTTAAAAAGTTTGGGGGCAGATTCTGAATTGG 536 | 537 GCTAAAAGACATGCATTTTTAAAACTAGGCAACTTCTTATTTCTTTC | 597 TAGCATTAAATCCCAAATCCTATTTAAAGACCTGACAGCATGAGAGACATCACTGCAT 656 | 657 TTATAGGACCTTCTGGTGGTTCTGCTGTTACGTTTGAAGTCTGACAATCCTTGAGAATCT 716 | 717 TTGCATGCAGAGGTAAGAGGTATTGGATTTTCACAGAGGAAGAACACACGCAGAAT 776 | 777 GAAGGGCCAGGCTTACTGAGGCTGTCCAGTGGAGGCTCATGGGTGGG | 837 AGGCAGCCTAGGGAGCCCAGTCCACTGAGCAAGCAAGGAACTGAGTGAG | 897 TTGCAGGAAAAGGCTAAGAAAAAGGAAAACCATTCTAAAACACAACAAGAAACTGTCCAA 956 | 957 AIGCITIGGGAACIGTGTTTATIGCCTATAATGGGTCCCCAAAATGGGTAACCTAGACTT 1016 | 1017 CAGAGAGAATGAGCAGAGAGAGAAATCTGGCTGTCCTTCCATTTTCATTCTGTT 1076 | 1077 ATCTCAGGTGAGCTGGAGGGGGACATTAGAAAAAAATGAAACAACAAAACAATTAC 1136 | 1137 TAATGAGGTACGCTGAGGCCTGTGTCTCTTGACTCCACTACTTAATTCCGTTTAGTGA 1196 | 1197 GAAACCTITCAAITTTCTITIAITAGAAGGGCCAGCTTACTGTTGGTGGCÀAAAITGCCA 1256 |

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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Center: Whitehead Institute/ MIT Center for Genome Research
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30493. 36518
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complement (36649. 36820)
36850. 37060
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43091. 43121
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| Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M. Direct Submission Direct Submission Submitted (Ge-Aug-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 03141, USA COMMENT On Aug 6, 2002 this sequence version replaced gi:14010820. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html | Sequencing vector: M13; M77815; 3% of reads Sequencing vector: Plasmid; n/a; 97% of reads Chemistry: Dye-terminator Big Dye; of reads Assembly program: Phrap; version 0.960731 Consensus quality: 180355 bases at least Q40 Consensus quality: 180355 bases at least Q30 Consensus quality: 18338 bases at least Q20 Insert size: 173000; agarose-fp Insert size: 183761; sum-of-confids Quality coverage: 7.8 in Q20 bases; agarose-fp Quality coverage: 7.8 in Q20 bases; agarose-fp Quality coverage: 7.8 in Q20 bases; agarose-fp veconsists of 7 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved. * 1055 1154: gap of 100 bp * 1055 2825: contig of 1671 bp in length * 2926 2925: gap of 100 bp * 2926 2925: gap of 100 bp * 2926 2948: contig of 26223 bp in length | 29248: gap of 100 bp 59090: contig of 29842 bp in 59190: gap of 100 bp 110096: contig of 50906 bp in 110196: gap of 100 bp 149104: gap of 100 bp 149304: contig of 39108 bp in 149404: gap of 100 bp 184361: contig of 34957 bp in catton/Qualifiers .184361 rganism="Homo sapiens" coll_type="genomic DNA" by Exef="taxcn:9606" hromosome="8" figh="8" cote="assembly_fragment" coe="assembly_fragment" |
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Homo sapiens homeobox protein NKX3.1 mRNA, complete cds.
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AF247704.1 GI:9963969
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94.7%; Score 1832.6;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1886; Conservative 0; Mismatches
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/note="sasembly_fragment
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RTSSQRQRDPEPEPEPEGGRSRAGAQNDQLSTGPRAAPEEAFTLAETEPERHLGSY
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LIKLTETQVKIAFQNRYTKTKRKQLSSELGDLEKHSSLPALKEBAFSRASLVSVYNSYP
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                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(Dases 1 to 3266)

Korkmaz, K.S., Korkmaz, C.G., Ragnhildstveit, E., Kizildag, S., Pretlow, T.G. and Saatioglu, F.
Pull-length cDNA sequence and genomic organization of human NKX3.1-Alternative mRNA forms and regulation by both androgens and
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Unpublished
E 2 (bases 1 to 3266)
S Korkmaz, K.S., Korkmaz, C.G. and Saatcioglu, F.
Direct Submission
Submitted (22-MAR-2000) University of Oslo, Bi
Oslo, Gaustadalleen 21, Oslo 0349, Norway
Location/Qualifiers
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/product=*homeobox protein NKX3.1"
/protein_id="AAG09781.1"
/db_xreff="GI:9963970"
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Pred. No. 0;
0; Mismatches
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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| QY 1480 TTCTTTCAACTTGCAATTTGCAAGGATTACACATTTCACTGTGATGTATATTGTGTTGCA 1539 Db 2865 TTCTTTCAACTTGCAATTTGCAAGGGTTACACATTTCACTGTGATGTATTGTGTTGCA 2924 QY 1540 GNGAAAAGAAAAAGTGTCTTTGTTTAAAATTACTTGGTTTGTGAATCCATCTTGCTTTT 1599 Db 2925AAAAAAAAAAAAGTGTCTTTGTTTAAAATTACTTGGTTTGTGAATCCATCTTGCTT 2979 QY 1600 TCCCCATTGGAACTACTTTAAAATTACTTGGTAGAAAACATCTGAAGAGCT 1659 Db 2980 TCCCCATTGGAACTAAACCATTAACCCATCTGGAAGACTGGTAGAAAACATCTGAAGAGCT 3039 | OY 1660 AGTCTATCAGCATCTGACAGGTGAATTGGATGCTTCTCAGAACCATTTCACCCAGACAGC 1719 | 1840 1840 3220 3220 344306/c 244306/c 201 101110N Se ESSION AR | | SOURCE SE COUNT IGIN Query Matc Best Loca Matches 1, | Db 1814 TGTTTTTTTTTTTTTTTTTCCCCCAAAGCTTTACCCTCTCAATTTTTTTT |

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Labrag, J., Astle, J.H., Carroll, E. III, Endege, W.O., Ford, D.N. Monahan, J.E., Schlegel, R. and Steinmann, K.E. Genes and gene expression products that are differentially regulated in prostate cancer
Patent: US 6476207-A 96 05-NOV-2002;
Location/Qualifiers
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Pred. No. 6.7e-142;
0; Mismatches 13;
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                                                                                                                                                                                                                         Sequence 96 from patent US 6476207.
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AR244068/c
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Zhang J., Astle, J.H., Carroll, E. III, Endege, W.O., Ford, D.M., Monahan, J.E., Schlegel, R. and Steinmann, K.E.
Regnes and gene expression products that are differentially regulated in prostate cancer
Patent: US 6476207-A 81 05-NOV-2002;
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Pred. No. 5.2e-145;
0; Mismatches 16;
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Search completed: August 26, 2003, 17:06:58 Job time : 9204 secs

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August 26, 2003, 11:05:41; Search time 642 Seconds (without alignments) 8140.361 Million cell updates/sec
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| SIDSI/gggdata/geneseqf.embl/NA1981.DAT: |
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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1: /SIDS1/gcgdata/g
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Maximum DB seq length: 200000000
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1936
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Diagnosing, monitoring, and staging prostate cancer

Cafferkey R;

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                     The present sequence represents a human prostate specific gene (PSG) (gene ID 244673). The mRNA levels for PSG are about 20 fold higher in the prostate than in other tissues. The PSG mRNA was found to be overexpressed in prostate tumour samples. The specification describes a method for diagnosing the presence of, or metastatic potential of prostate cancer in a patient. The method comprises measuring PSG levels in a cell, tissue or bodily fluid sample of the patient and a control the patient compared to the control is associated with the presence of, the patient compared to the control is associated with the presence of or metastasis of prostate cancer. The method can also be used for staging prostate cancer in a patient. The methods are used to detect, monitor, stage and give a prognosis for prostate cancer.
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The present invention describes isolated polypeptides, comprising an immunogenic portion of a prostate tumour protein (PTP). The polypeptides and polymucleotides encoding them have cytostatic activity and can be used in vaccines and in gene therapy. The polypeptides and polymucleotides encoding them, antigen presenting cells which express polymucleotides encoding them, antigen presenting cells which express comprising them can be used for inhibiting the development of prostate cancer in a patient. The polypeptides can be used to generate antibodies or anti-idiotypic antibodies for inhibiting the development of prostate the polymucleotides encoding the polypeptides can be used as a probe or to modulate the expression of the polypeptides. AAA066241 to AAA06691 and AAA08200 represent sequences used in the exemplification of
                                                                                                                                                             Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:335.
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                       GAATCTCCGCTTGTCCAAGACAGGGGCCTAAGGAGGTCTCCACACTGCTGCTAGGGCT
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the diagnosis and treatment of cancer, especially prostate cancer
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Carter
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 335-336; 579pp; English.
; 2000US-0570737.
; 2000US-0593793.
; 2000US-058783.
; 2000US-0651236.
; 2000US-0651279.
; 2000US-0657479.
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Best Local Similarity 99.0%;
Matches 1897; Conservative (
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| 1561 TGTTTAAAATTACTTGGTTTGTGAATCCATCTTGCTTTTTCCCCATTGGAACTAGTCATT 1620 2620 TGTTTAAAATTACTTGGTTTGTGAATCCATCTTGCTTTTTCCCCATTGGAACTAGTCATT 2679 2680 AACCCATCTCTGAACTGGTAGAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACGG 1739 2680 AACCCATCTCTGAACTGGTAGAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGG 1740 | RESULT 4 AM93680 standard; CDNA; 2984 BP. XX AM93680; XX AM93580; XX AM93680; XX AM93680; XX Whiman prostate-specific CDNA sequence P705P. XX COCT-2001 (first entry) XX COCD-2001 (first entry) XX MAN-2001; 2001W0-U801574. XX |
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| 1487 CCTCGCTTATTTAGCCGAGATCTGGTCTTTTTTTTTTTTTTTT | AGCCTAGGCCCTGGGGAGCCCAGTCCACTGAGCAGGAGCAGGAGGACTGAGTGAG |

1020 2080 ABGAAAAGGAAAACCATTCTAAAACACAACAAGAAACTGTCCAAATGC 2020 1260 2320 1440 ACGTGCTGCTGACACCGGACTACTAGCCAGCACAAAAGGCAGGG 1380 1560 2619 1620 NACTGGTAGAAAAACATCTGAAGAGCTAGTCTATCAGCATCTGACAGG 1680 2799 1800 CTITCIGCICITIACATITCITITAAAATAAGCATITAGTGCTCAGTC TTTCACTGTGATGTATATGTGTTGCAGNGAAAAAGAAAAAGTGTCTT TIGGITIGGAATCCATCTTGCTTTTTCCCCCATTGGAACTAGTCATT TCTCAGAACCATTCACCCAGACAGCCTGTTTCTATCCTGTTTAATA TCTCTACATGCATAACAAACCCTGCTCCAATCTGTCACATAAAAGTC

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                                                             Human, prostate cancer, therapy, diagnosis, cat eye syndrome,
chromosome 22q11.2, prostate-specific protein, chromosome 1,
prostate specific antigen, PSA, ss.
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                                 prostate-specific cDNA sequence P705P/9-F3
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ID, Retter MW, Stolk JA,
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Best Local Similarity 99.0%;
Matches 1897; Conservative
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prostate cancer;
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The present invention describes an isolated polypeptide (I) comprising at least an immunogenic portion of a prostate tumour antigen protein or its variant. (I) have cytostatic activity and can be used in vaccine production. (I), prostate tumour antigen polynucleotides, an antigen

Claim 50; Page 219; 276pp; English.

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presenting cell (APC e.g. a dendritic cell) that expresses (I), and a pharmaceutical composition containing (I) are useful for inhibiting the development of cancer in a patient. Antibodies specific for prostate specific proteins and oligonucleotides that hybridise to a polynucleotide that encodes a prostate specific protein are useful for detecting the presence or absence of a cancer or monitoring the progression of a cancer, especially prostate cancer. AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences used in the exemplification of the present invention.
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                                         TTTGGGAACTGTGTTTATTGCCTATAATGGGTCCCCAAAATGGGTAACCTAGACTTCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                Polypeptide comprising part of the Wilm's Tumour gene product sequence is used in the diagnosis and treatment of malignant diseases e.g. leukemia and cancer associated with WTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes compositions comprising peptides derived from the Wilm's tumour protein WT1 and methods for their use in treating malignant diseases. Peptides derived from both the murine and human WT1 proteins are provided. The human WT1 gene is found on chromosome 11p13, and the protein was shown to be a zinc finger transcription factor. The immunogenic peptides of the invention are particularly useful in the diagnosis and treatment of cancer and leukaemia. The present sequence is a coding sequence used in the exemplification of the invention.
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Carter D;
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                                                                                                                                                                                                                                                                                                                                                            New prostate-specific polynucleotides for diagnosing and tre diseases, in particular prostate cancer, and as markers for progression of cancer
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A, Day CH, Vedvick TS,
spler WT, Henderson RA;
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GR, Retter MW, Stolk JA, Day CH
Wang A, Skeiky YAW, Hepler WT,
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Best Local Similarity 99.0%;
Matches 1897; Conservative
02-OCT-2000; 2000US-0679426.
10-OCT-2000; 2000US-0685166.
                                   XU J.
DILLON D C.
MITCHAM J I.
HARLOCKER S L.
JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
STOLK J A.
DAY C H.
CARTER D.
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CARTER D.
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SKEIKY Y A W.
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Li SX,
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                       TGTTTAAAATTACTTGGTTTTGTGAATCCATCTTGCTTTTTTCCCCATTGGAACTAGTCATT
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04-OCT-2000; 2000US-0679272.
28-MAR-2001; 2001US-0822827.
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MITCHAM J L.
HARLOCKER S I
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RETTER M W.
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KALOS M D.
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(HEND/)

HURAL J. MCNEILL P D.

STOLK J A.
DAY C H.
VEDVICK T S.
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WANG A.
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                                                                                                                                                                             immunogenic portions, useful for diagnosing, preventing and/or treating cancer, particularly prostate cancer .
                                                                                                                                                                                                                                                              The invention describes a fusion protein comprising at least one amino acid sequence of immunogenic portions of any of the 3 sequences not defined in the specification, or sequences having at least 70 or 90 $ sequence identity to any one of the 35 sequences defined in the USPTO defined in the specification. The fusion protein, composition and particularly prostet cancer. The fusion protein, composition and particularly prostet cancer. The proteins are useful as markers to indicate the presence or absence of cancer. This sequence represents a prostate cancer therapy associated CDNA.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent of the contact.
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                                                                 Kalos MD;
Carter D;
Hural J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 25; Length 2984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Indels
                                                         Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA, I PD, Houghton RL, Y De Bassols CV, Foy TW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2984 BP; 837 A; 659 C; 645 G; 842 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            seqdata.uspto.gov/sequence.html?DocID=US20020192763.
                                                                                                                                                                            New fusion protein comprising prostate-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 94.9%; Score 1836.4; I Best Local Similarity 99.0%; Pred. No. 0; Matches 1897; Conservative 0; Mismatches
                                                                                                                                                                                                                                     Example 3; SEQ ID NO 335; 85pp; English.
 HOUGHTON R L.
Y DE BASSOLS C V.
FOY T M.
                                                                                                                                WPI; 2003-352711/33.
P-PSDB; ABU71662.
                                                          Xu J, Dilloo
Fanger GR, J
Li SX, Wang
Mcneill PD,
 (HOUG/) H
(DBAS/) N
(FOYT/) H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                               (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient (f) assessing the prostate cell carcinogenic potential of a compound;
                                                                                                 2740 TGAATTGGATGGTTCTCAGAACCATTTCACCCAGACAGCCTGTTTCTATTAATA
                                                                                                                                               1741 AATTAGTTTGGGTTCTCTACATGCATAACAAACCCTGCTCCAATCTGTCACATAAAAGTC
                                                                                                                                                                                                                                 2860 IGIGARATITAGICAGCACCCCCACCAACTITAITITCTAIGIGITITITITGCA
                                                  2680 AACCCATCTCTGAACTGGTAGAAAAACATCTGAAGAGCTAGTCTATCAGCATGTGACAGG
                                                                                  TGAATTGGATGGTTCTCAGAACCATTTCACCCAGACAGCCTGTTTCTATCCTGTTTAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid molecule (I) compa nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; prostate cancer; cytostatic; carcinogen; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression marker cDNA 25130
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16-MAR-2000; 2000US-189862P.
25-MAY-2000; 2000US-207454P.
9-UJN-2000; 2000US-211314P.
18-JUL-2000; 2000US-21914P.
13-DEC-2000; 2000US-255281P.
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determining whether prostate cancer has metastasized in a patient assessing the aggressiveness or indolence of prostate cancer in a
                                                                              1 AATGGTATGCCAACTTAAAGTATTTACAGGGTGGCCCAAATAGAACAAGATGCACTCGCTG
                                                                                                GAATCTCCGCTTGTCCAAGACAGGGCCTAAGGAGGGTCTCCACACTGCTGGTAAGGGGT
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                                           Query Match 83.9%; Score 1624.6; DB 23; Length 3227; Best Local Similarity 92.4%; Pred. No. 0; Matches 1752; Conservative 0; Mismatches 134; Indels 10; C
                                                                                                                                                                                                      301 GAAAGGCAACAIAAITCIICCIICCIICTIIIAAAAIIITGIGIICCII
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BP. standard; cDNA; 3228 us-09-700-700-1.rng

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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) alecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate call carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastaaized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATGGTATGCCAACTTAAGTATTTACAGGGTGGCCCAAATAGAACAAGATGCACTCGCTG 1381
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(I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                      cytostatic, carcinogen; pharmacodyanamic gene; ss.
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Pred. No. 0;
0; Mismatches 129; Indels
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                                     CDNA 22884
                                                                                                                                                                                                                                                                                                                                                                                              PREDICTIVE MEDICINE
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                                     Human prostate expression marker
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2000US-207454P.
2000US-211314P.
2000US-219007P.
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Best Local Similarity 92.6%;
Matches 1757; Conservative
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pharmacogenomic
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gene; ss.
2638 ATGITCAATGCCACGTGCTGACACCGACCGGAGTACTAGCCAGGCACAAAAGGCAGGG
              --TCTTTGTTTAAAATTACTTGGTTTGTGAATCCATTGCTTTTTTCCCCATTGGAACTA
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ID ABV23209 standard; cDNA; 3228
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16-MAR-2000; 2000US-189862P.
25-MAY-2000; 2000US-207454P.
09-UUN-2000; 2000US-211314P.
18-UUL-2000; 2000US-219007P.
13-DEC-2000; 2000US-255281P.
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pharmacogenomic marker;
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The invention relates to an isolated nucleic acid molecule (I) comprising appecification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
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Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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(I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
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Pred. No. 0;
0; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                          Sequence 3228 BP; 879 A; 740 C; 765 G; 829 T; 15 other;
                                                                 Claim 1; Page 4176; 11750pp; English.
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Matches 1757; Conservative (
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3058 TTAAAAAAATAATTGGGGGTTTTTAACAGGAAAAAAACCCTGGTCCAATTTGGCCAAAA 3117
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate call carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                              Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
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                                                          3118 AAAATTTGGGAATTGGAATTTAATTCACCCCCCCCCACAAATTTTAATTTTCCAAGGGGTT
                               12; Gaps
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                                                                                                         3178 TTTTGGCAACAAAAAGGGTTTGAAAAAAAAAGCCCCC 3215
                                                                                        TITITGCAACATATGAGTGTTTTGAAAATAAAGTACCC 1890
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Best Local Similarity 92.6%;
Matches 1757; Conservative C
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16-WAR-2000; 2000US-1896G2P.
25-WAY-2000; 2000US-207454P.
09-UUN-2000; 2000US-21314P.
18-JUL-2000; 2000US-219007P.
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                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) ablecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cal carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
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Matches 1757; Conservative
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(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                        1 AATGGTATGCCAACTTAAGTATTTACAGGGTGGCCCCAAATAGAACAAGATGCACTCGCTG
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                                                                                                                       also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                     Query Match
Best Local Similarity 92.6%; Pred. No. 0;
Matches 1757; Conservative 0; Mismatches 129; Indels 12;
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                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid molecule (I) comprising a nuclectide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer; cytostatic; carcinogen; pharmacodyanamic marker;
marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                   --TCTTTGTTTAAAATTACTTGGTTTTGTGAATCCATCTTGCTTTTTTTCCCCATTGGAACTA
                                                           cciritirgiaaaaactigggigggaaccartiggiritirccccifgaaccr
                                                                                    GTCATTAACCCATCTCTGAACTGGTAGAAAACATCTGAAGAGCTAGTCTATCAGCATCT
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16-MAR-2000; 2000US-189862P.
25-MAY-2000; 2000US-207454P.
09-UJM-2000; 2000US-211314P.
18-JUL-2000; 2000US-219007P.
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| 1 AGCCTAGGCCCTGGGGAGCCCAGTCCACTGAGCAAGCAAG | 1 AGGAAAAGGCTAAGAAAAAGGAAAACCATTCTAAAACAAAAGAAACGAAGGAACTGTCCAAATGC | 1 TITGGGAACTGTGTTTATTGCCTATAATGGGTCCCCAAAATGGGTAACCTAGACTTCAGA | 1 GAGAATGAGCAGAGGAAAGGAGAAATCTGGCTGTCCTTCCATTTTCATTGTTATGT | 1 CAGGTGAGCTGGTAGAGGGGAGACATTAGAAAAAAATGAAACAACAAAACAATTACTAAT | 1 GAGGTACGCTGAGGCCTGGGAGTCTCTTGACTCCACTACTTAATTCCGTTTAGTGAGAAA | 1 CCTTTCAATTTTCTTTTATTAGAAGGCCAGCTTACTGTTGGTGGCAAAATTGCCAACAT 1 | 1 AAGTTAATAGAAAGTTGGCCAATTTCACCCCATTTTCTGTGGTTTGGGCTCCACATTGCA | 1 AIGITCAAIGCCACGIGCTGACACCGACCGGAGTACTAGCCAGCACAAAAGGCAGGG 1 | 1 TAGCCTGAATTGCTTTCTGCTCTTTACALTTCTTTAAAATAAGCATTTAGTGCTCAGTC 1 | 1 CCTACTGAGTACTCTTTCTCTCCCTCCTGAATTTAATTCTTTCAACTTGCAATTTGC 1 | 1 AAGGATTACACATTTCACTGTGATGTATTGTGTTGCAGNGAAAAGAAAA | 7TCITIGITTAAAATTACTIGGITIGIGAATCCATCTIGCTTTTCCCCATIGGAACTA 1 | S GICATTAACCCATCTCTGAACTGGTAGAAAACATCTGAAGAGGTAGTCTATCAGCATCT 1 | S GACAGGIGAATIGGAIGGITCTCAGAACCAITICACCCAGACAGCCTGITTCTAICCIGT 1 | 5 TIAAIAAATIAGTTTGGGTTCTCTACATGCAIAACAAACCCTGGTCCAATCTGTCACATA 1 | S AAAGTCTGTGACTTGAAGTTTAGTCAGCACCCCACCAAACTTTATTTTTCTATGTGT 1 | 3 TTTTGCAACATATGAGTGTTTTGAAATAAAGTACCC 1890 |
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-352-149A-335
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US-09-328-475C-96
US-09-328-475C-96
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US-09-328-475C-14
US-09-328-475C-14
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                                            2620 TGTTTAAAATTACTTGGTTTGTGAATCCATCTTGCTTTTTCCCCATTGGAACTAGTCATT
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Sequence 335, Application US/09352616A

Patent No. 6395278

APPLICANT: Dillon, Davin C.

APPLICANT: Dillon, Davin C.

APPLICANT: Dillon, Davin C.

APPLICANT: Micham, Jangchun

APPLICANT: Micham, Jangchun

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS

TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE

CURRENT APPLICATION NUMBER: US/09/352,616A

NUMBER OF SEQ ID NOS: 472.

SOFTWARE: FASESEO FOR FOR
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99.0%; Pred. No. 0;
cive 0; Mismatches
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; ORGANISM: Homo sapien
US-09-352-616A-335
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LENGTH: 2984
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                                                                        TTACTCACTAAAGGGCTTCATTTTAGTCCAGATTTTTAGTCTGGCTGCACCTAATG
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                  2261 CCTTTCAATTTTCTTTTATTAGAAGGGCCAGCTTACTGTTGGTGGCAAAATTGCCAACAT
                                                            1261 AAGTTAATAGAAAGTTGGCCAATTTCACCCCATTTTCTGTGGGTTTGGGCTCCACATTGCA
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| Sequence 335, Application US/09232149A
| Patent No. 6465611
| GENERAL INPORMATION:
| APPLICANT: V. Jianghun
| APPLICANT: Dillon, Davin C.
| APPLICANT: Mitcham, Jennifer Lynn
| TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
| TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
| FILE REFERENCE: 210121.427C6
| CURRENT FILING DATE: 1999-01-15
| NUMBER OF SEQ ID NOS: 338
| SOFTWARE: FastSEQ for Windows Version 3.0
| SEQ ID NO 335
| LENGTH: 2984
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Pred. No. 0;
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Best Local Similarity 99.0%;
Matches 1897; Conservative C
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ORGANISM: Homo
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; Sequence 81, Application US/09328475C
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ORGANISM: Homo Sapien
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71.7%; Score 1388.8;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1438; Conservative 1; Mismatches
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SEQ ID NO 334
LENGTH: 2051
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LOCATION: (1)...(2051)
OTHER INFORMATION: n = A,T,C
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ORGANISM: Homo sapien
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32.5%; Score 628.4; DB 4;
Best Local Similarity 97.4%; Pred. No. 1.3e-164;
Matches 678; Conservative 0; Mismatches 13;
                   CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SEQ ID NO 96
LENGTH: 1024
TYPE: DNA
ORGANISM: Homo Sapien
FEATURE:
                                                                                                     NAME/KEY: misc_feature
i LOCATION: (1)...(1024)
i OTHER INFORMATION: n = A,T,C or G
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Sequence 96, Application US/09328475C

Sequence 96, Application US/09328475C

Sequence 96, Application US/09328475C

Sequence 96, Application US/09328475C

SERVERAL INFORMARTION:

APPLICANT: Shang Vinmy

APPLICANT: Carroll III, Eddie

APPLICANT: Fordege, Wilson O.

APPLICANT: Schlegel, Robert

APPLICANT: Schlegel, Robert

APPLICANT: Schlegel, Robert

TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER

TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER

CURRENT APPLICATION NUMBER: US/09/328,475C
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                                             Length 1024;
                                Query Match
33.1%; Score 641.2; DB 4; Length:
Best Local Similarity 97.3%; Pred. No. 3.8e-168;
Matches. 681; Conservative 0; Mismatches 16; Indels
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US-09-328-475C-81
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         572 CTTATTTCTTTTAAAAATACATAGCATTAAATCCCAAATCCTATTTAAAGACTGA
                                                           CAGCTTGAGAAGGTGACTACTGCATTTATAGGACCTTCTGGTGGTTCTGCTGTTACGTTT
                                                                        GAAGTCTGACAATCCTTGAGAATCTTTGCATGCAGGAGGTAAGAGGTATTGGATTTTC
                                                                                                                                                        752 ACAGAGGAAGAACAGAGGGGGAAAATGAAGGGCCAGGCTTAACTGAGGCTGTCCAGTGGAGG
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US-09-328-475C-82
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731 AGGTGAACTGGTAAAAGGGAGACATTTGAAAAAATGAAACNACCAAAACCATTACTAAT 790
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                                                                                                                                                                                                                                                                                                                     APPLICANT: Zhang, Jimmy
APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTALLY REGULATED IN PROSTATE CANCER;
FILE REFERENCE: 1532.002/200130.463
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
SECTION OF SE
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                                                                                                                                                                                                                                             Sequence 95, Application US/09328475C Patent No. 6476207 GENERAL INFORMATION:
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NAME/KEY: misc_feature

LOCATION: (1)...(1024)

COTHER INFORMATION: n = A,T,C or (US-09-328-475C-95)
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ORGANISM: Homo Sapien
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APPLICANT: Carroll III, Eddie
APPLICANT: Endege, wilson O.
APPLICANT: Endege, wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Schlegel, Robert
APPLICANT: Stelmann, Kathleen E.
APPLICANT: Stelmann, Kathleen E.
TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
FILE REFERENCE: 1532.002/200130.463
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1024)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 94.9
Matches 690; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo Sapien
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| Db 572 GCATTTATMGGACCTTCTGGTGTTTTGCTGTTTTGAAGTCTGACAATCCTTGAGA 513 Qy 713 ATCTTTGCAGAGGAGGTATTGGATTTTCCAGAGGAACACCAGGGC 772 | 0. 8-475C-23 Ce 23, Application US/09328475C No. 6476207 L INFORMATION: CANT: Zhang, Jimmy CANT: Astel, Jon H. CANT: Carroll III, Eddie CANT: Brdege, Wilson O. CANT: Monahan, John E. CANT: Schlegel, Robert | HE FIFT IN THE SEE TO SEE THE SEE THE SEE TO |
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| QY 933 AAAACACAACAAGAAACTGTCCAAATGCTTTGGGAACTGTGTTTATTGCCTATAATGGGT 992 Db 577 AAAAAACAACAAGAAACTGTCCAAATGCTTTGGGAACTGTTTATTGCCTATAATGGGT 636 QY 993 CCCCAAAATGGGTAACTAGAGAGAATGAGAAGAGAGAAACAGAGAAATTGGT 636 Db 637 CCCCAAAATGGGTAACTTAGAAATGAGAATGAGAATGAGAAATTGGAAATTGGAAATTGGAAATTGAAAATGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAAATTGAGAAATTGAGAAATTGAGAAATTGAGAAATTGAGAAATTGAGAAATTGAGAAATTGAAAATTGAAATTGAAATTGAGAATTGAGAATTGAGAAATTGAAAATTGAAATTGAAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGAGAATTGATAATTGAGAATTGAGAATTGAGAATTGAGAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAA | 111LE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER CURRENT APPLICATION NUMBER: US/09/328,475C CURRENT APPLICATION NUMBER: US/09/328,475C CURRENT FILING DATE: 1999-06-09 NUMBER OF SEQ ID NOS: 341 SOFTWARE: Fast SEQ for Windows Version 3.0 ILENGTH: 1013 TYPE: DNA ORGANISM: Homo Sapien FRATURE: NAME/KEY: misc_feature COCATURE: NAME/KEY: misc_featu | Query Match |

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GTCCCCAAAATGGGTAACCTAGACTTCAGAGAAGAATGAGCAGAGAGGAAAGGAGAAATCT 1050
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APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Bridge, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: QUARRER DIFFERENTIALLY REGULATED IN PROSITATE CANCER
FILE REFERENCE: 1532.002/200130.463
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SEQ ID NOS: 341
LENGTH: 744
                                                                                                                                                                   720 AAGTINGGGGCCAGAIICIGAAII-GGIIAAAAGACAIGCAIIITIAAAACIAGCAACIC
                                                                                                                                                                                                                                                                                           631 ACAGCTTGAGAAGGTCACTACTGCATTTATAGGACCTTCTGGTGGTTCTGCTGTTACGTT
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                                             Length
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                                                                                                                            511 AAGTTTGGGGGCAGATTCTGAATTGGGCTAAAAGACATGCATT
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                                           Score 582.2; DB 4;
Pred. No. 7.4e-152;
0; Mismatches 10;
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                                           Query Match 30.1%;
Best Local Similarity 97.6%;
Matches 622; Conservative
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US-09-328-475C-318/c
    US-09-328-475C-319
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APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Caracil III, Eddie
APPLICANT: Caracil III, Eddie
APPLICANT: Caracil III, Eddie
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: ARE DIFFERENTALLY REGULATED IN PROSTATE CANCER
FILE REFERENCE: 1532.002/200130.463
CURRENT APPLICATION NUMBER: US/09/328,475C
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 341
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 319
LENGTH: 720
                                                                                ACTICTTATITICTITICADABATACATAGCATTAAATCCCAAATCCTATITAAAGGC
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                                                                                                                                                                                       CTGACAGCTTGAGAAGGTCACTACTGCATTTATAGGACCTTCTGGTGGTTCTGGTGTTAC
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                              AAAAAGTTTGGGGGCAGATTCTGAATT-GCCTAAAAGACATGCATTTTTAAAAACTAG
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US-09-328-475C-319/c
Sequence 319, Application US/09328475C
Parent No. 6476207
GENERAL INFORMATION:
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LOCATION: (1)...(720)
OTHER INFORMATION: n = A,T,C or
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ORGANISM: Homo Sapien
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42; Indels
                                                                                                                                                                                 Query Match 27.9%; Score 539.6; DB 4; Best Local Similarity 92.7%; Pred. No. 5.7e-140; Matches 635; Conservative 0; Mismatches 42;
CURRENT APPLICATION NUMBER: US/09/328,475C CURRENT FILING DATE: 1999-06-09 NUMBER OF SEQ ID NOS: 341 SEQ ID NO 19 SEQ ID NO 19 LENGTH: 980
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                                                                                                                                   ; LOCATION: (1)...(980)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-19
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Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
                                                                                                                     NAME/KEY: misc feature
LOCATION: (1) ... (980)
                                                                             TYPE: DNA
ORGANISM: Homo Sapien
FEATURE:
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US-09-439-313-434
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Fatent No. 6475C307
FAPLICANT: Alang, Jimmy
FAPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Schlegel, Robert
APPLICANT: FILE OF INVENTION: ARE DIFFERENTIALIX REGULATED IN PROSTATE CANCER
FILE REFERENCE: 1532.002/200130.463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  937 CACAACAAGAAACTGTCCAAATGCTTTGGGAACTGTGTTTATTGCCTATAATGGGTCCCC
                                                                                                                               Gaps
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                                                                                                    Length 744;
                                                                                                                         7; Indels
                                                                                             30.0%; Score 581; DB 4; I 98.1%; Pred. No. 1.6e-151; Live 0; Mismatches 7;
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CTHER INFORMATION: n = A,T,C or G
US-09-328-475C-318
                                                                                       Query Match
Best Local Similarity 98.1
Matches 619; Conservative
                      NAME/KEY: misc_feature
 ORGANISM: Homo Sapien
FEATURE;
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Length 980
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Mitcham, Jennifer Lynn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Michael
APPLICANT: Retter, Mark
APPLICANT: Retter, Mark
APPLICANT: Bay, Craig
TITLE OF INVENTION: DAY, Craig
CURRENT APPLICANTON: DAY, Craig
TITLE OF INVENTION: DAY, Craig
TITLE OF INVENTION: DAY, Craig
TITLE OF INVENTION: DAY, Craig
TITLE OF STORMER: 1999-11-12
CURRENT APPLICATION NUMBER: US/09/439,313
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 434
LENGTH: 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        24.2%; Score 469.4; DB 4; 99.2%; Pred. No. 1.2e-120; tive 0; Mismatches 1;
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Patent No. 6395278
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqui
APPLICANT: Xi, Jiangchun
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.2
Matches 483; Conservative
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; ORGANISM: Homo sapiens
US-09-439-313-434
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US-09-352-616A-434
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TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1.999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FREESQ for Windows Version 3.0
SEQ ID NO 434
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Job time : 176 secs
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Sequence 23, Appl Sequence 319, App Sequence 318, App

Sequence 68, Appl Sequence 19, Appl Sequence 76, Appl Sequence 77, Appl Sequence 434, Appl Sequence 634, Appl Sequence 78, Appl Sequence 78, Appl Sequence 102, Appl Sequence 103, Appl Sequence 103, Appl Sequence 222, Appl Sequence 103, Appl Sequence 115, Appl

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Run on:

Sequence:

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APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: BEDIECT, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
Score 1836.4;
Pred. No. 0;
0; Mismatches
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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Vedvick, Thomas S
Carter, Darrick
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Best Local Similarity 99.0
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ORGANISM: Homo sapien
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   GENERAL INFORMATION:
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-012-896-335
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| 2141 1141 2201 1201 2261 | Oy 1261 AAGTTAATAGAAAGTTGGCCAATTTCACCCCATTTCTGTGGTTTGGGCTCCACATTGCA | QY 1381 TAGCCTGAATTGCTTTTCTTTTTAAAATAAGCATTTAGGCCTCAGTC | 1501 | 1561 2620 | OY 1621 AACCCATCTGAACTGGTAAAAACATCTGAAAAGCTAGTCTATCAGCATCTGACAGG - 2680 AACCCATCTGAACTGGTAGGAAACATCTTGAACTGTTTTTTTT | 2740 | 2800 | 2860 | OY 1861 ACMTATGAGTGTTTTGAAATDAAGTACCCATGTCTTTATTAAAAAAAAAA | RESULT 2 US-09-780-669-335 ; Sequence 335, Application US/09780669 : Datent No Resultant | GENERAL INFORMATION: APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C. APPLICANT: Michael C. | APPLICANT: MICCABM, Jennier L. APPLICANT: Harlocker, Susan L. APPLICANT: Jiang, Yuqui APPLICANT: Henderson, Robert A. | APPLICANT: Kalos, Michael D. APPLICANT: Fanger, Gary R. APPLICANT: Retter, Marc W. APPLICANT: Stolk, John A. APPLICANT: Day, Craig H. APPLICANT: Vedvick, Thomas S. |
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| AATGGTATGCCAACTTAAGTATTTACAGGGTGGCCCAAATAGAACAAGATGCACTCGCTG 60 | 181 GTTGCATTTTTTATTAGTAGAAAGGCCTCTTCTCAACTTTTTTCCCTTGGGC 240 1247 GTTGCATTTTTTTTATTAGTAGAAAGGCCTCTTCTCAACTTTTTTCCCTTGGGC 1306 241 TGGAGAATTTAGAATCAGAAGTTTCCTGGAGTTTTTCAGGCTATCATATACTGTATCCT 300 1307 TGGAGAATTTAGAATCAGAAGTTTCCTGGAGTTTTTCAGGCTATCATATACTGTATCCT 300 1307 TGGAGAATTTAGAATCAGAAGTTTCCTGGAGTTTTCAGGCTATCATATATAT | CAGCAA CAGCAA CTTATG | | | | 01 ATTAATCCCAATCCTATTTAAAGACCTGACAGCTTGAGAAGGTCACTACTGCATTAT | 5 2 5 | 721 ATGCAGAGGAGGTAAGAGTATTGGATTTTCACAGAGGAAGAACACGGGGGAGAATGAAG 780 | 781 GGCCAGGCTTACTGAGGCTGTCCAGTGGACGCTCATGGGACATGGAAAAGAAGGC 840 | | | 961 TITGGGAACTGTGTTTATTGCCTATAATGGGTCCCCAAAATGGGTAACCTAGACTTCAGA 1020 | 1021 GAGAATGAGCAGAGGGAGAAAGAAATCTGGCTGTCCTTCCATTTTCATTGTTATCT 1080 2081 GAGAATGAGCAAAGGAGAAATCTGGCTGTCCTTCCATTTTCATTCTGTTATCT 1080 2081 GAGAATGAGCAAAGGAGAAATCTGGCTGTCCTTCCATTCTGTTATCT 2140 1081 CAGGTGAGCTGGTAGAGGGAGACATTAGAAAAATGAAAAAAAA |

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APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hepler, William
APPLICANT: Hepler, William
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPERENCE: 210121.427624
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 335.
                                                                                                                                                                                                                                                         DB 9;
                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                      Query Match 94.9%; Score 1816.4; Best Local Similarity 99.0%; Pred. No. 0; Matches 1897; Conservative 0; Mismatches
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US-09-780-669-335
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| | RESULT 3 US-09-822-827-335 IS Sequence 315, Application US/09822827 Sequence 315, Application US/09822827 GENERAL INFORMATION: TITLE OF INVENTION: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER CURRENT APPLICATION NUMBER: US/09/822,827 IURBER OF SEQ ID NOS: 982 SOFTHARE: PastSEQ for Windows Version 3.0 SEQ ID NO 335 LENGTH: 2984 TYPE: DNA CURRANISM: Homo sapien US-09-822-827-335 | Duery Match Best Local Smilarity 94.9%; Score 1836.4; DB 9; Length 2984; Matches 1897; Conservative 0; Mismatches 12; Indels 7; Gaps 5; 1 AATGGRANGCCAACTTAAGTATTACAGGGGGCCCAAAAAAAAAAAA |

| 1545 CAAAGCTTTATCTGTCTTGACTTTTTAAAAAGTTTGGGGGCAGATTCTGAATT-GGCTA 1603 | 721 ATGCAGGGGGGGGTAAGGGTATTGCAGGGGGGGGGGGGG |
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| Qy 1741 AATTAGTTTGGGTTCTTACATGCATAACAAACCCTGCTCCCAATCTGTCACATAAAAGTC 1800 Db 2800 AATTAGTTTGGGTTCTCTACATGCATAACAAACCCTGCTCCAATCTGTCACATAAAAGTC 2859 Qy 1801 TGTGACTTGAAGTTTAGTCAGCACCCCCACCAACTTTATTTTTTTT | U. O. 122-80-315 Application US/09233880 Publication US/09233880 Publication US/09232880 Publication US/09232880 Publication US/09232880 Publication US/09232881 Publication US/09232881 Publication US/09232881 Publication US/09232881 Publication US/09232882 Publication US/092328 Publication US/09238 Public |

| 1157 GAATCTCCCCTGTCCAAGACGCCCCTAAGAGGCCTCCACACTCTCCACAGGCCCCAAGACCACGCCCCCACAGGCCCCCACAGGCCCCCACAGGCCCCCC | 0077 4440000000000000000000000000000000 |
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| AACCCATCTCTGAACTGGTAGAAAACATCTGAAGAGGTAACCATCTCTGAACTGGTAGAAAACATTCGAACATCGTAGAACACTTTCACCCAGACAGCGTAATTGGATCGTTCTCAGAACCATTTCACCCAGCAGCGCTGATTGGATTCTCAGAACCATTTCACCCAGCAGCGTGTACAACACTTTCACCCAGCAGCGTGTTTTTATTGTTTTAGTTTTAGTTTTAGTTTTAGTTTTAGTTTTAGTTTTAGTTTAGTTTTAGTTTTAGTTTTAGTTTTAGTTTAGTTTAGTTTAGTTCAGAACTTTTATTAGTTTAGTTTAGTTTAGTTCAGAACTTTTATTAGTTTAGTTCAGAACTTTTATTAGTTTAGAAATTAAGTTACCCAACTTTATTAGTTCAAAATTAAGTTACCCAACTTTATTAGTTCAAAATTAAGTTACCCAACTTTATTAGTTCAAAATTAAGTTACCCAACTTTATTAGTTCAAAATTAAGTTACCCAACTTTATTAGTTCAAAATTAAGTTACCCAACTTTATTAGTTCAAAATTAAGTTACCCAACTTTATTAGTTCAAAATTAAAGTACCCAACTTTATTAGTTCAAAATTAAAGTACCCAACTTTATTAGTTCAAAATTAAAGTACCCAATGTTTTTAGTTCAAAATTAAAATAAAGTACCCAATGTTTTTAGTTCAAAATTAAAATAAAGTACCCAATGTTTTTAGTTCAAAATTAAAATAAAGTACCAATGTTTTAGTTCAAAATTAAAAGTACCAATAGAATTAAAATAAAATAAAATAAAATAAAATAAAATAAAAATAAAA | |
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                                              AND
              APPLICANT: Foy, Teresa
APPLICANT: Forger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY ITITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER.
FILE REFERENCE: 210121.427026
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILLNG DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 335
LENGTH: 2984
                                                                                                                                                                                                                                               Query Match 94.9%; Score 1836.4; DB 10; Lengt
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1897; Conservative 0; Mismatches 12; Indels
   Vinals de Bassols, Carlota
                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapien
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                                                           AAGTTAATAGAAAGTTGGCCAATTTCACCCCATTTTCTGTGGTTTTGGGCTCCACATTGCA
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                 2261 CCTTTCATTTTATTAGAAGGCCAGCTTACTGTTGGTGGCAAATTGCCAACAT
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Publication No. US20020193296A1
GENERAL INFORMATION:
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APPLICANT: Nitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Garter, Day, Craig H.
APPLICANT: Garter, Day Craig H.
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Skelky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
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US-09-895-814-335
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1 AATGGTATGCCAACTTAAGTATTTACAGGGTGGCCCCAAATAGAACAAGATGCACTCGCTG
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APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Pay, Teressa
APPLICANT: Fay, Teressa
APPLICANT: Mantanabe, Yoshihiro
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Wangher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS F
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CAN,
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CAN,
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CAN,
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011-12-10
SEQ ID NO 335
LENGTH: 2884
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99.0%; Pred. No. 0;
iive 0; Mismatches
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                                                                               Sequence 335, Application US/10012896
Publication No. US20020183251A1
GENERAL INFORMATION:
                                                                                                                    APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Micham, Jennifer L.
APPLICANT: Micham, Jennifer L.
APPLICANT: Micham, Jennifer L.
APPLICANT: Giang, Yugiu
APPLICANT: Ralos, Michael D.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
                                                                                                                                                                                                                                                                                    Wang, Aijun
Skeiky, Yasir A.W.
Hepler, William T.
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Best Local Similarity 99.0
Matches 1897; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-335
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| | RESULT 6 Sequence 315, Application US/10010940 Sequence 315, Application WS/10010940 SPENICANT: Dilanghum APPLICANT: Harlocker, Susan Louise APPLICANT: Reed, Steven G. APPLICANT: Reed, Steven G. APPLICANT: Solv. Adont APPLICANT: Solv. Addont APPLICANT APPLICANT |
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| | AGCCTAGGCCCTGGGCGCCCCAGTCCACTGGCAAGCAAGGAACTGAGTGAG |

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| | | 1441 CTACTGAGTACTCTTTCTCCCCCTCTGAATTTAATTCTTTCAATTGC 1500 2501 CTACTGAGTACTTCTCTCCCCTCTCTGAATTTAATTCTTTCAATTGC 1500 2501 CCTACTGAGTACTCTTCTCCCCTCCTCTGAATTTAATTCTTTCAATTTGC 2560 2501 AAGGATTACACTTCACTGTATATTGTTTGCATTTTTTTTT | 2501 1561 2620 1621 | Db 2680 AACCCATCTCTGAACTGGTAGAAAACATCTGAAGGCTGTCTATCAGCATTTTTTTT | | 1801 | Oy 1861 ACATAFGAGTGTTTGAAAATAAAGTACCCATGTCTTTATTAAAAAAAA | RESULT 9 US-10-205-823-282 Sequence 282, Application US/10205823 Publication No. US20030108963A1 GENERAL INFORMATION: APPLICANT: Schlegel, Robert Monaham Tahn Tahn | APPLICANT: Endege, Wilson O. APPLICANT: Ganavarapu, Manjula APPLICANT: Ganavarapu, Manjula APPLICANT: Gorbatcheve, Bella APPLICANT: Kamatkar, Shubhangi APPLICANT: Wangela M. APPLICANT: Wangela M. | ; APPLICANT: Zhao, Xumei.; ; APPLICANT: Zhao, Xumei.; ; APPLICANT: Anderson, Dustin ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND ; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND FITLE OF INVENTION: THERAPY OF PROSTATE CANCER. | FILE KEFERENCE: MRI-044 CURRENT APPLICATION NUMBER: US/1 CURRENT FILING DATE: 2002-07-25 PRIOR APPLICATION NUMBER: 60/377 PRIOR FILING DATE: 2001-07-25 PRIOR APPLICATION NUMBER: 60/314 |
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| 121 GAATCTCGGCTTGTCCAAGACAGGGGCCTAAGGAGGGTCTCCACACTGCTGCTGGGGGCT 180 1187 GAATCTCCGCTTGTCCAAGACAGGGGCCTAAGGAGGGTCTCCACACTGCTGCTTGTCCAAGGGCCT 1246 181 GTTGCATTTTTTATTAGTAGAAAGTGGAAAGGCCTCTTCTCAACTTTTTTCCCTTGGGC 240 1247 GTTGCATTTTTTTTTTATTAGTAGAAAGGCCTCTTCTCAACTTTTTTCCCTTGGGC 240 1247 GTTGCATTTTTTTTTTTATTAGTAGAAAGTGGAAAGGCCTCTTCTCAACTTTTTTCCCTTGGGC 240 | 241. TGGAGAATTTAGAATCAGAAGTTTCCTGGAGTTTTCAGGCTATCATATATACTGTATCCT 300 | |) 00 4- | 1604 AAAGACATGTATTTAAAACTAGCAACTCTTATTCTTTCCTTTAAAAATAGC 1661 601 ATTAAATCCCAAATCCTATTAAAGACCTGACAGGCATTGAGAAAGGTCACTACTGCATTATA 60 1662 ATTAAATCCCAAATCCTATTTAAAGACCTGACAGGTCAGAGGTCACTACTGCATTAT 660 | TTTGC | 721 ATGCAGAGGATAAGAGGTATTGGATTTTCACAGAGGAAGAACACAGGGCAGAATGAAG 780 | 781 GGCCAGGCTTACTGAGGCTGTCCAGTGGAGGGCTCATGGGTGGG | ### ### ############################## | 961 TTTGGGAACTGTGTTATTGCCTATAATGGGTCCCCAAAATGGGTAACCTAGACTTCAGA 1020 [| 1081 CAGGTGAGCTGGTAGAGGGGAGACATTAGAAAAAATGAACAACAACAAACA | 1111 |

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| PRIOR FILING DATE: 2001-08-22 PRIOR APPLICATION NUMBER: 60/35,020 PRIOR APPLICATION NUMBER: 60/35,020 PRIOR PILING DATE: 2001-09-25 PRIOR PELICATION NUMBER: 60/341,746 PRIOR FILING DATE: 2001-12-12 PRIOR PELICATION NUMBER: 60/362,158 PRIOR FILING DATE: 2002-03-05 NUMBER OF ERQ ID NOS: 455 SOFTWARE: FESTESQ for Windows Version 4.0 SEQ ID NO 282 LENGTH: 3266 TYPE: DNA TYPE: DNA ORGANISM: Homo sapiens US-10-205-823-282 | Query Match Best Local Similarity 95.8%; Pred. No. 0; Matches 1826; Conservative 0; Mismatches 47; Indels 34; Gaps 12 | 1 AATGGTATGCCAACTTAAGTATTTACAGGTGGCCCAAATAGAACAAGATGCACTCGCTG 60 | 61 IGATTITAAGACAAGCIGTATAAACAGAACTCCACTGCAAGAGGGNGGGCCGGGCCAGGA 120 | 121 GAATCTCCGCTTGTCCAAGACAGGGCCTAAGGAGGGTCTCCACACTGCTGCTAGGGGCT 180 | 2 4 | | GAAAGGCAACATAATTCTTCCTTCCCTCTTTAAAATTTTGTGTTCTTTTTGCAGCAA | TTACTCACTAAAGGGCTTCATTTTAGTCCAGATTTTTAGTCTGGTGCACCTAACTTATG | CCTCGCTTATTTAGCCCGAGATCTGGTCTTTTTTTTTTT | 481 CAAAGCTTTATCTGTCTTGACTTTTTAAAAAGTTTGGGGGAGATTCTGAATTGGGGTA 540 | AAAGACATGCATTTTTAAAACTAGGCAACTTCTTATTTCTTTTCCTTTAAAAATACATAGC | ATTABATCCCAAATCCTATTTABAGACCTGACAGCTTGAGAA-GGTCACTACTGCATTTA 6 | TAGGACTITCIGGIGGITCTGCTGTTACGTTTGAAGTCTGACAATCTTGAGAATCTTTG 7 | CATGCAGAGGAAGGAATTGGATTTTCACAGA-GGAAGAACACGGGAGATGA 7 CATGCAGAGGAACACAGGGGAATTTTCACAGA-GGAAGAACACAGGGGAAGAA CATGCATTTTCACAGA-GGAAGGAACACAGGAAGAACAAGGAAGAATTGGATTTTCACAGAGGAAGAAGAAAAAAAA | AGGCCAGGCTTACTGAGGCTGTCCAGTGGAGGCTCATGGGAGAAGAAG |

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1169 GACTCCACTACTTAATTCCGTTTAGTGAGAACCTTTCAATTTTCTTTTATTAGAAGGGC 1228
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Sequence 334, Application US/1020193

Publication No. US20020192699A1

APPLICANT: Chang, Jimmy

APPLICANT: Astel, Jon H.

APPLICANT: Ended, Wilson O.

APPLICANT: Ended, Wilson O.

APPLICANT: Schlege, Wilson O.

APPLICANT: Schlegel, Robert

APPLICANT: Schlegel, Robert

APPLICANT: Schlegel, Robert

APPLICANT: Schlegel, Robert

TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER

TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE

TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE

CURRENT APPLICATION NUMBER: 2002-07-23

CURRENT APPLICATION NUMBER: 2002-07-23

SOFTWARE: FARENEE OF SEQ ID NOS: 341

SOFTWARE: FARENEE OF SEQ ID NOS: 341

SOFTWARE: PARENEE OF SEQ FOR WINGOWS VERSION 3.0

LENGTH: 2051
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                                                                                                                                                                                                                                                                                                                                             Score 1388.8; Pred. No. 0; 1; Mismatches
                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: n = A,T,C or G
US-10-202-193-334
                                                                                                                                                                                                                                                                                                                                       Query Match 71.7%;
Best Local Similarity 98.8%;
Matches 1438; Conservative
                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapien
               US-10-202-193-334/c
                                                                                                                                                                                                                                                                                            LOCATION:
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Sequence 258, Application US/09925300
Patent No. US20020151681A1
Patent No. US20020151681A1
APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION:
FILE REFERENCE: PA101

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CTGAGCAAGCAAGGGACTGAGTGAGCCTTTTGCAGGAAAAGGCTAAGAAAAAGGAAAACC 927
                                                                  APPLICANT: Zhang, Jimmy
APPLICANT: Astel, Jon H.
APPLICANT: Astel, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Brdege, Wilson O.
APPLICANT: Ford, Donna M.
APPLICANT: Monahan, John E.
APPLICANT: Steinmann, Kathleen E.
TITLE OF INVENTION: GENEERRYIALLY REGULATED IN PROBUCTS THAT
TITLE OF INVENTION: GENEERRYIALLY REGULATED IN PROSTATE CANCER
FILE REFERENCE: PP-01532.103/200130.463D1
CURRENT PELLICANT: S103/20130.463D1
CURRENT PELLICAN NUMBER: US/10/202.193
CURRENT FILING DATE: 2002-07-23
NUMBER OF SEQ ID NOS: 341

LENGTH: 1024
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           Sequence 81, Application US/10202193
Publication No. US20020192699A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(1024)

OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo Sapien
                              Publication No. US20
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      568
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CURRENT FILING DATE: 2001-08-10
FRIOR APPLICATION NUMBER: PCT/US00/05988
FRIOR FILING DATE: 2000-03-08
FRIOR APPLICATION NUMBER: 60/124,270
FRIOR FILING DATE: 1990-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PatentIn Ver. 2.0
SOFTWARE: 7850 ID NOS 288
LENGTH: 755
                                                                                                                                                                                                                                                                                                  ; NAME/KEY: misc feature
i LOCATION: (755)
; OTHER INCORMATION: n equals a,t,g, or
US-09-925-300-258
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 35.4%;
Best Local Similarity 98.9%;
Matches 700; Conservative
                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                    992 TCCCCAAAATGGGTAACCTAGACTTCAGAGAATGAGCAGAGAGAAAGGAGAAATCTG
                                                               TAAAACACAACAACAAAACTGTCCCAAAATGCTTTTGGGAACTGTGTTTATTGCCTATAATGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Acted, John H.

APPLICANT: Acted, John H.

APPLICANT: Endege, Wilson O.

APPLICANT: Endege, Wilson O.

APPLICANT: Ford, Donna M.

APPLICANT: Ford, Donna M.

APPLICANT: Schlegel, Robert

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Pred. No. 1.6e-160;
0; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       AAAAATGAAACAACAATTACTAATGAGGTAC 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 82, Application US/10202193
Publication No. US20020192699A1
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// LOCATION: (1)...(1024)

// OTHER INFORMATION: n = A,T,C or G

US-10-202-193-82
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Best Local Similarity 94.9%;
Matches 690; Conservative
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ORGANISM: Homo Sapien
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| APPLICANT: Astel, Jon H. |
| APPLICANT: Astel, Jon H. |
| APPLICANT: Carroll III, Eddie |
| APPLICANT: Bridge, Wilson O. |
| APPLICANT: Ford, Donna M. |
| APPLICANT: Monahan, John E. |
| APPLICANT: Schlegel, Robert |
| APPLICANT: Robert |
| AP
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32.5%; Score 628.4; DB 13
Best Local Similarity 97.4%; Pred. No. 1.5e-160;
Matches 678; Conservative 0; Mismatches 13;
                                                                                                                                                                                                                                                                                Sequence 96, Application US/10202193
Publication No. US20020192699A1
GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or G
US-10-202-193-96
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US-10-202-193-95
; Sequence 95, Application US/10202193
; Publication No. US20020192699A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Batel, Jon H.
; APPLICANT: Ford, Donna M.
; APPLICANT: Ford, Donna M.
; APPLICANT: Schlegel, Robert
; APPLICANT: Schlegel, Robert
; APPLICANT: Schlegel, Robert
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
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; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; CURRENT FILING DATE: 2002-07-23
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                  611 TTGGGAACTGTGTTTATTGCCTATAATGGGTCCCCCAAAATGGGTAACCTAGAGTTTCAGAG
                                                                                                                                                            GGAAAAGGCTAAGAAAAAGGAAAACCATTCTAAAACACAACAAGAAACTGTCCAAATGCT
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Pred. No. 8.1e-159;
0; Mismatches 30;
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; OTHER INFORMATION: n = A,T,C or G
US-10-202-193-95
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Best Local Similarity 95.0%;
Matches 690; Conservative (
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ORGANISM: Homo Sapien
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LENGTH: 1024
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                             218 TTATTTCTTTCCTTTAAAATACATAGCATTAAATCCCAAATCCTATTTAAAGACCTGAC
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                                                                                                 AGCTTGAGAAGGTCACTACTGCATTTATAGGACCTTCTGGTGGTTCTGCTGTTACGTTTG
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                                                                                                                                                                                                           AAGTCTGACAATCCTTGAGAATCTTTGCATGCAGGGGGGGTAAGAGGTATTGGATTTTCA
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Search completed: August 26, 2003, 20:43:56
Job time : 581 secs

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BUG19261 UI-H-FH1-CA430303 UI-H-FL1-AA813266 a144903.8 BQ018482 UI-H-DH1-BE97355 601680918 AIS9273 2 prosect BF679599 602154041 AIS20178 tu54a11.X AA528104 ni15a05.8 AA431255 nj09a12.8 BA431255 nj09a12.8 BA437224 zv54b10.8 BQ236596 AGENCOLR

A1620178 AA528104 AA531255 AA437224 BQ230696 BF965018

Sequence:

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Run

BE772782 AI989281

AA516531 AA442287 AA640241 AA972883 AA809587 AA707108 AI139031 AI052805 AI791607 AI571633 AI685682

BM983868 BQ020946 AW886523 BUG19261 CA430903 AA813266 BQ018482 BC973555

112 113 12 10 10 10 10 10 10

AA516531 nh52900.r AA442287 zv54b10.r AA442287 zv54b10.r AA672883 zv54b10.r A1989281 10 prosta A860958 nj43e11.8 AA707108 zj33a03.8 A1139031 qc22e12.x A1791607 nc32a05.y A1571633 tr86f06.x A1571633 tr86f06.x A1557413 pr2.1 A1557413 pr2.1 A1557413 tr86f06.x A1557413 pr2.1 1.2 A1557413 sh1855676 603383255 AA649358 nr28d08.r AA533772 nj93c05.8

AI557413 BF855203

AA229495

AA640928 AI525269 AA531606 AA493522 BF855210 RC3-FN020 BF855199 RC3-FN020 AI027196 ov83a09.x

BF855210 BF855199

ALIGNMENTS

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BX102941 BX102941 Soares testis NHT Homo sapiens cDNA clone IMAGP998M201862; IMAGE:757435, mRNA sequence.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Bbert, L., Hell, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
Radelof, U., Schneider, D. and Korn, B.
Human Unigeneset - RZPD3
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CBB53124 UI-CF-FNO
BUG01144 AGENCOURT
BUG22196 UI-H-FHI-
                                                                                                                                                August 26, 2003, 13:36:36; Search time 4917 Seconds (without alignments) 9569.548 Million cell updates/sec
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                                                                                                                                                                                                                                                                                      1 aatggtatgccaacttaagt.....gggcggccgccgactagtga 1936
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                               22781392 segs, 12152238056 residues
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Listing first 45 summaries
                                                                                                         nucleic search, using sw model
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em_gas_phg: *
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gb_gas2: *
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Result Š.

Database

Minimum I Maximum I

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/organism="Homo sapiens"
//wol_type="mRNA"
//db_xxef="texon:9606"
//clone="UJ-CF-RNO-467-a-06-0-UT"
//issue_type="Human Lung Epithelial cells"
//lab_host="BHIOB (Life Technologies) (Tl phage resistant)"
//lab_host="DHIOB (Life Technologies) (Tl phage resistant)"
//clone lib="UJ-CF-FNO"
//clone lib-Taxy was subtracted according to according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, benco-soaresemica.
                                                                       1261 AAGTTAATAGAAAGTTGGCCAATTTCACCCCATTTTCTGTGGTTTGGGGTCCACATTGCA 1320
                                                                                                                                                                                                                                                                           CB853124
BIJ bp mRNA linear EST 22-APR-2003
UI-CF-FN0-afq-a-06-0-UI.SI UI-CF-FN0 Homo sapiens cDNA clone
UCF-FN0-afq-a-06-0-UI 3', mRNA sequence.
                    Email: paul_mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [Dases 1 to 813]

Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            University of Iowa 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA Tel: 319 356 4866
Fax: 319 356 7171
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                                                                                                                                           1321 ATGTTCAATGCCACGTGCTGCTG 1343
                                                                                                                                                                               720 Argerchargecaccieriscre 742
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178 c 164 g
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CB853124.1 GI:30048262
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Seq primer: M13 FORWARD
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: McCray, PB
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                                                                                                                                                                                                                        Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
Ml3r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTGGGAACTGTGTTTATTGCCTATAATGGGTCCCCAAAATGGGTAACCTAGACTTCAGA 1020
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Pred. No. 1.9e-106;
0; Mismatches 2; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                          1. .742
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGP998M201862; IMAGE:757435"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.6%;
99.6%;
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Matches 740; Conservative
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/ Organism==nmano baplens ...
/ forgatism==nmano baplens ...
/ mol type="mrkNa"
/ db_xref='taxon:9606"
/ clone='InAngE:445018"
/ lab host."DH108 (T1-phage-resistant) "
/ clone_lib="winkNa" | lab host."DH108 (T1-phage-resistant) "
/ clone_lib="winkNa" | lab host."DH108 (T1-phage-resistant) "
/ clone lib="winkNa" | lab host."Dh10 | lab host."Dh10
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  DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/Link at: http://image.llnl.gov plate: LicMA5672 row: c column: 19 High quality sequence stop: 481. Location/Qualifiers
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Pred. No. 2.8e-100;
0; Mismatches 37;
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Best Local Similarity 94.8%;
Matches 744; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 851)

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National Institutes of Health, Mammalian Gene
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: NCI
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UI-CF-DU1-aaw-b-04-0-UI.s1 UI-CF-DU1 Homo sapiens cDNA clone
UI-CF-DU1-aaw-b-04-0-UI 3', mRNA sequence.
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Homo sapiens
Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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Pred. No. 6.4e-100;
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                                                                                                                                                                                                                                                                                                                                                       BU622196 700 bp mRNA linear EST 23-SEP-2002 UI-H-FH1-bfu-m-08-0-UI.81 NCI CGAP_FH1 Homo sapiens cDNA clone PIT-H-1-bfu-m-08-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained Seq primer: M13 FORWARD
POLYA=Yes.
    ACAAAAGGCAGGGTAGCCTGAATTGCTTTTCTGCTTTTACATTTCTTTTAAAATAAGCAT 1427
                                                                                                                                                                                    1547 GAAAAAGIGICTTIGITIAAAATIACTIGGITIGIG--AAICCAICTIGCITITICCC 1604
                                        601
                                                                                 662 ACTIGCAAITIGCAAGGGAIACCAITITCACIGGGGAIGIAITAITIGGGIIGCAAAAAAA 721
                                                                                                                                                                                                            722 AAAAAGGGCTTTGTTTAAAATACTTGGGNTTGGGAAATCCCTCCTGCTTTTTTCCC 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo. 1 (bases 1 to 700)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
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Unpublished
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AUTHORS
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UI-H-DH1-axh-j-06-0-UI.81 NCI_CGAP_DH1 Homo sapiens CDNA clone IMAGE:5828837 3', mRNA sequence. BQ020946 BQ020946.1 GI:19756232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1840 TTTTTCTATGTGTTTTTTGCAACATATGAGTGTTTTGAAAATAAAGTACCCATGTCTTTA 1899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbe-remail.nib.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LiML at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
sequence: 1.30, AT rich#Low_complexity (matched compliment)
POLYA-YES.
                                                                                                                                                                                                                                      318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 TGTTTCTATCCTGTTTAATAAATTAGTTTGGGTTCTCTACATGCATAACAAACCCTGCTC 138
                                                                                                                                                                                                                                                                                                                                            317 CCCCATTGGAACTAGTCATTAACCCATCTCTGAACTGGTAGAAAAAACATCTGAAGAGCTA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                  257 GTCTATCAGCATCTGACAGGTGAATTGGATGGTTCTCAGAACCATTTCACCCAGACAGCC 198
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                494 TAAGCATTTAGTGCTCAGTCCCTACTGAGTACTCTTTTTTCTCCCCTCCTCTGAATTTAAT
                                                                                                                   434 TCTTTCAACTTGCAATTTGCAAGGATTACACATTTCACTGTGATGTATATTGTGTTGCA-
                                                                                                                                                                                   1541 NGAAAAGAAAAAAGTGTCTTTGTTAAAATTACTTGGTTTGTGAATCCATCTTGCTTTTT
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dev_stage="Adult"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:5828837"
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/tissue_type="Primary Lung Epithelial Cells"
/dev_stage="Manutum"
/lab host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-DUI"
/note="Organ: Lung; Vector: pT773-pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-CF-DUI is a normalized CDNA library containing the following tissue(s): Primary Lung Epithelial Cells The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTTTGGGCTCCACATTGCAATGTTCAATGCCACGTGCTGCTGACCGGACCGGAGTACT 1360
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                                                                                                                                                                                                                                                                                                                                                          Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Banto Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com) or from Open Biosystems
The following repetitive elements were found in this CDNA
Seq primer: M13 FORWARD
POLYA-Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (1 (bases 1 to 674)
Bonaldo,M.F., Lemon,G. and Soares,M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGTGGCAAAATTGCCAACATAAGTTAATAGAAAGTTGGCCAATTTCACCCCATTTTCTGT
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                            Contact: McCray, PB
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AUTHORS
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/ Mod_type="mRNN"

/ dbv zref="taxon:9606"

/ dev_stage="mRNN"

/ dov_stage="mRNN"

/ dov_stage="mRNN and institute for Cancer Research) profiles

into the pUC 18 vector. Reverse transcription of tissue

mRNN amd cDNA amplification were performed under low

stringency conditions."

96 a 145 c 163 g 174 t
                      AW886523 678 bp mRNA linear EST 23-MAY-2000
                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases I to 678)
Dias Neto,E., Garcia,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RCI-OT0083-220
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGAAAAGGCTAAGAAAAAGGAAAACCATTCTAAAACACAACAAGAAACTGTCCAAATGC 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITIGGGAACTGTGTTTATTGCCTATAATGGGTCCCCAAAATGGGTAACCTAGACTTCAGA
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                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Pred. No. 5.9e-86;
0; Mismatches 15;
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Location/Qualifiers
                                                            AW886523.1 GI:8048535
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97.4%;
                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: +55-11-2704922
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631; Conservative
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                                                                                                                                                   Homo sapiens
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/lab host="DH10B (Life Technologies)"
/clone lib="NCI_CGAP_DH1"
/hore="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR 1; Site 2: Not 1;
NCI_CGAP_DH1 is a normalized cDNA library containing the following tissue(8): VS-8 Cell line from Metastatic Chondrosarcoma in Lung. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dr primer containing a Not 1 site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dr)18 tail. The sequence tag for this library is AGATCATTGC.

TAG IISBUI-H-DH1

TAG IISBUI-H-DH1

TAG IISBUI-H-DH1

TAG IISBUI-H-DH1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.9%; Score 617; DB 12;
98.2%; Pred. No. 1.2e-88;
iive 0; Mismatches 8;
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Best Local Similarity 98.2
Matches 644; Conservative
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TTTGGGAACTGTGTTTATTGCCTATAATGGGTCCCCAAAATGGGTAACCTAGACTTCAGA

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I, and cloned directionally into pT7T3-Pac vector. The oligomuclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not site and the (dT)18 tail. The sequence tag for this library is AGAATCCGGC. The cell line was provided by Dr. James Martin from the University of
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UI-H-FL1-bge-i-17-0-UI.s1 NCI CGAP_FL1 Homo sapiens cDNA clone
UI-H-FL1-bge-i-17-0-UI 3', mRNA sequence.
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      cDNA was ligated to an EcoR I adaptor, digested with Not
                                                                                                                                                                        TAG LIB=UI-H-FH1
TAG_TISSUB=Human Chondrosarcoma Cell Line CS8 - Grade 1
Chondrosarcoma
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Pred. No. 8.3e-86;
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Best Local Similarity 99.3%;
Matches 601; Conservative
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CA430903/c
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Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
POLYA-Yes.
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/lab_host="DH108 (Life Technologies)"
/lab_host="DH108 (Life Technologies)"
/lab_host="DH108 (Life Technologies)"
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The library was constructed and normalized according to Bonaldo, Lennon and Soares, Genome Research, 6791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded
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UI-H-FH1-bfr-b-10-0-UI.81 NCI CGAP FH1 Homo sapiens cDNA clone
UI-H-FH1-bfr-b-10-0-UI 3', mRNA sequence.
                                                                  CAGGTGAGCTGGTAGAGGGGAGACATTAGAAAAAATGAAACAACAAAAATACTAAT 1140
                                                                                                                                                      GAGGTACGCTGAGGCCTGGGAGTCTCTTGACTCCACTACTTAATTCCGTTTAGTGAGAAA 1200
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1 (bases 1 to 608)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP);

Tumor Gene Index
                                                                                          CAGGTGAGCTGGTAGAGGGGAGACATTAGAGAAAAAACAACAACAATTACTAAT
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/organism="Homo sapiens"
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Contact: Robert Strausberg, Ph.D.
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1587 CCATCTIGCTITTTCCCCATIGGAACTAGICATTAACCCATCTCTGAACTGGTAGAAAA 1646
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Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D.,
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/dev gtage="waute"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
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/clone_lib="waute"
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I; NCI_CGAP FILI is a normalized cDNA library derived from
a pool of mRNA obtained from 4 cell lines from grade III
chondrosarcoma tissues. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
sith an oligo-dT primer containing a Not I site. Double
with Not I, and cloned directionally into pT773-Pac
vector: The oligonucleotide used to prime the synthesis of
list-strand cDNA contains a library tag sequence that is
sequence tag for this library is GAGGTCGGTG. The cell
University of Lowa.
TAG ILSUB-HUFIL

TAG I
                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.

Email: Gapbs.remail.nih.gov

Tissue Procurement: James Martin

CDN Library preparation: Dr. M. Bento Soares, University of Iowa

CDN Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained

Seq primer: M13 FORWARD

POLYA-yes.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 631)
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                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
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/organism="Homo sapiens"
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1647 CATCTGAAGAGCTAGTCTATCAGCATCTGAGAGAGATTGGATGGTTCTCAGAACCATT 1706
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335 CCATCTTGCTTTTCCCCATTGGAACTAGTCATTAACCCATCTCTGAACTGGTAGAAAAA 276
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp//image.html
Insert Length: 982 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 503.
Location/Qualifiers
1.599
/organism="Homo. sapiens"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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                                                                                                                                                                                GGCTCCACATTGCAATGTTCAATGCCACGTGCTGCTGACACCGGACCGGAGTACTAGCCAG
                                                                                                                                                                                                                   1367 CACAAAAGGCAGGGTAGCCTGAATTGCTTTCTGCTCTTTACATTTCTTTTAAAATAAGCA
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                                                                                                           Gaps
by Bento Soares and M. Fatima Bonaldo.
131 g 168 t
                                                                                                           5,
                                                                       Length 599;
                                                                     Score 582.2; DB 9; Length
Pred. No. 4.3e-83;
0; Mismatches 3; Indels
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
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                                                                 Query Match 30.1
Best Local Similarity 99.2
Matches 596; Conservative
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/tissue_trype="Metastatic Chondrosarcoma"
/dev_etage="Metastatic Chondrosarcoma"
/dev_etage="Metastatic Chondrosarcoma"
/lab_host="UBHIOB (Life Technologies)"
/clone_lib="NCI_CGAP_DHII"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_l: Site_l: Site_l: Not I;
NCI_CGAP_DHI is a normalized cDNA library containing the following tissue(8): VS-8 Cell line from Metastatic Chondrosarcoma in Lung. The library was constructed according to Bonaldo, Lennon and Soarces, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor; digested with Not I, and cloned directionally into pT7T--pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGATCATTGC.
TAG_IIB-UI-H-DHI
TAG_IIB-UI-H-DHI
TAG_IIS-UI-H-DHI
TAG_
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cDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov The following repetitive elements were found in this cDNA sequence: 1-30, AT_rich#Low_complexity (matched compliment) Seg primer: M13 FORWARD
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0; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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1148

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Tall (Dases 1 to 563)

S Zhang, J.S. and Smith, D.I.
High throughput screening for androgen regulated genes in LNCaP cells: Identification of hAG-2 as an androgen regulated gene over to unpublished

Contact: Zhang, Jin-San
Contact: Zhang, Jin-San
Mayo Clinic Cancer Cencer
200 lst St. SW, Rochester NN 55905, USA
Fal: 507-2663131
Fax: 507-2663193
Email: zhang, jinsan@mayo.edu.
Small: zhang, jinsan@mayo.edu.
Location/Qualifiers

Location/Qualifiers
                                                                                                        GCAGAGAGCAAAGGAGAAATCTGGCTGTCCTTCCATTTTCTGTTATCTCAGGTGAG 1088
                                                                                                                                                                                                                            CTGAGGCCTGGGAGTCTCTTGACTCCACTTAATTCCGTTTAGTGAGAAACCTTTCAA 1208
                  GCTAAGAAAAAGGAAAACCATTCTAAAACACAACAAGAAACTGTCCAAATGCTTTGGGAA 120
                                                                        1209 TITICITITATTAGAAGGGCCAGCTTACTGTTGGTGGCAAAATTGGCAACATAAGTTAAT 1268
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prostate cancer cell line LNCaP Homo sapiens cDNA, mRNA sequence.
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subtracted cDNA libraries from prostate cancer cell line
LNCaP treated with androgen."
                                             969 CTGTGTTTATTGCCTAAAAGGGTCCCCAAAATGGGTAACCTAGACTTCAGAGAGAATGA
                                                                                                                                                                   CTGGTAGAGGGAGACATTAGAAAAAATGAAACAACAAAACAATTACTAATGAGGTACG
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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CAGAACCATITCACCCAGACAGCCTGTTTCTATCCTGTTTAATAAATTAGTTTGGGTTCT 170
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                            CTACATGCATAACAAACCCTGCTCCAATCTGTCACATAAAAGTCTGTGACTTGAAGTTTA
                                                    169 CTACATGCATAACAAACCCTGCTCCAATAAAAAGTCTGTGAATTTA
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Parayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can http://image.lln.gov
Clone distribution: MGC clone distribution information can http://image.lln.gov
Plate: LLCM818 row: d column: 05
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                                                                                                                                              Plate: LLCM018 row: d column: 05
High quality sequence stop: 614.
Location/Qualifiers
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/clone="IMMGE:4294931"
/lab_host="DH10B (T1 phage-resistant)"
/clone=lb="UNH MGC 83"
/note="Organ: NH MGC 83"
/note="Organ: procedure power: pDNR-LIB (Clontech);
Site 1: Sfil (ggccgcctcggcc); Site 2: Sfil (ggccattatggcc ); Site 1: Sfil (ggccattatggcc ); Site 2: Sfil (ggccattatggcc ); Site 1: Sfil (ggccattatggcc ); Si and 3' adaptors were used in cloning as follows: 5' adaptors sequence: 5'-CACGGCCATATGGCC.3' and 3' adaptor sequence: 5'-ATTTAGAGCCGAGCGCGCGCCGACAGCG-TY ). Average insert size 1:4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
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99.5%; Pred. No. 4.4e-75;
iive 0; Mismatches 0;
     Plate: LLCM1145 row: a column: 12
High quality sequence stop: 563.
Location/Qualifiers
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                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Matches 565; Conserv
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 565)
                                                                                                                                                                                                                                                                                                                                                                 Unpublished
Contact: Robert Strausberg, Ph.D.
Email: Gapba-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 6e-78;
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BF679599.1 GI:11953494
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Best Local Similarity 99.8%;
Matches 561, Conservative
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/lab host="DH10B"
/clone_lib="MCI CGAP Pr28"
/note="Organ: prostee; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCT CGAP Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
Subtraction by Bento Soares and 1217928-1220615).
8 a 84 c 113 g 151 t and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                          CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
found through the I.M.A.G.B. Consortium/LINL at:
Insert Length: 825 Std Brror: 0.00
High quality sequence stop: 456
POLYM=NO.
                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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27.0%; Score 521.8; DB 9; Length 538;
Best Local Similarity 99.1%; Pred. No. 1.96-73;
Matches 536; Conservative 0; Mismatches 2; Indels 3
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/mol_type="mRNA"

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/clone="IMAGE:2254844"
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   AI620178
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                                                  Homo sapiens (human)
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